



SEQUENCE LISTING

<110> KERE, Juha

<120> NOVEL HUMAN GENE FUNCTIONALLY RELATED TO DYSLEXIA

<130> 0933-0214P

<140> US 10/681,199

<141> 2003-10-09

<160> 42

<170> PatentIn Ver. 2.1

<210> 1

<211> 1263

<212> DNA

<213> Homo sapiens

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<223> coding sequence for human DYXC1 (cDNA)

<400> 1

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<213> Homo sapiens

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<222> (369)..(1628)

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Thr Ala Val Phe Leu Ser Leu Pro Leu Lys Gly Val Cys Val Arg Asp
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Thr Asp Val Phe Cys Thr Glu Asn Tyr Leu Lys Val Asn Phe Pro Pro
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Lys Ala Lys Ile Gly Asn Asp Thr Ile Val Phe Thr Leu Tyr Lys Lys
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gaa gcg gcc atg tgg gag acc ctt tct gtg acg ggt gtt gac aaa gag 650
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gca aaa gaa gct aca gaa gca aaa gct gca gca aag cgg gaa gat caa 746
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Lys Tyr Ala Leu Ser Val Met Met Lys Ile Glu Glu Glu Glu Arg Lys
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aaa ata gaa gat atg aaa gaa aat gaa cgg ata aaa gcc act aaa gca 842
Lys Ile Glu Asp Met Lys Glu Asn Glu Arg Ile Lys Ala Thr Lys Ala
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Gly Thr Glu Leu Lys Ser
415          420

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<213> Homo sapiens

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Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Arg Ala Lys
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Lys Glu Asp Ser Ile Pro Ala Pro Arg Ser Val Gly Ser Ile Lys Ile 225 230 235 240		
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Ala Glu Glu Glu Glu Trp Leu His Lys Gln Ala Glu Ala Arg Arg Ala 260 265 270		
Met Asn Thr Asp Ile Ala Glu Leu Cys Asp Leu Lys Glu Glu Glu Lys 275 280 285		
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His Val Arg Arg Gly Thr Ala Phe Cys Gln Leu Glu Leu Tyr Val Glu 370 375 380		
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Arg Asn Trp Glu Asn Ile Phe Pro Glu Lys Leu Lys Glu Asp Arg Val	
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Val Phe Pro Thr Ala Leu Arg Glu Ser Gln Val Ala Glu Glu Glu Glu	
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Pro Glu Phe Phe Asp Leu Lys Glu Glu Arg Asn Pro Asp Trp Leu	
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Val Asp Ala Tyr Asn Leu Ala Ile Arg Leu Asn Cys Lys Ile Pro Leu	
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<213> Mus musculus
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Val Phe Cys Gly Glu Ser Tyr Leu Lys Val Asn Phe Pro Pro Phe Leu
      35          40          45

Phe Glu Leu Phe Leu Tyr Ala Pro Ile Asp Asp Gly Lys Ser Lys Ala
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Lys Ile Gly Asn Asp Thr Ile Leu Phe Thr Leu Tyr Lys Lys Glu Pro
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Val Leu Trp Asp Ser Leu Ser Val Pro Gly Val Asp Lys Glu Met Met
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Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Lys Ala Lys
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Glu Ala Thr Glu Ala Lys Ala Val Ala Lys Arg Glu Asp Gln Arg Tyr
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<213> Homo sapiens

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<220>

<223> Description of Artificial Sequence: RT-PCR primer

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caagctgagg cacgaagagc aatga

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<211> 1263

<212> DNA

<213> Pan troglodytes

<220>

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gtc	ttt	ctg	tct	ctg	ccc	ctc	aaa	ggc	gtg	tgc	gtc	aga	gac	acg	gac	96
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gtg	ttc	tgc	atg	gaa	aac	tat	ctg	aag	gtc	aac	ttt	cct	cca	ttt	tta	144
Val	Phe	Cys	Met	Glu	Asn	Tyr	Leu	Lys	Val	Asn	Phe	Pro	Pro	Phe	Leu	
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ttt	gag	gca	ttt	ctt	tat	gct	ccc	ata	gac	gat	gag	agc	agc	aaa	gca	192
Phe	Glu	Ala	Phe	Leu	Tyr	Ala	Pro	Ile	Asp	Asp	Glu	Ser	Ser	Lys	Ala	
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Lys	Ile	Gly	Asn	Asp	Thr	Ile	Val	Phe	Thr	Leu	Tyr	Lys	Lys	Glu	Ala	
	65				70				75					80		

gcc	atg	tgg	gag	acc	ctt	tct	gtg	acg	ggg	gtt	gac	aaa	gag	atg	atg	288
Ala	Met	Trp	Glu	Thr	Leu	Ser	Val	Thr	Gly	Val	Asp	Lys	Glu	Met	Met	
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caa	aga	att	aga	gaa	aaa	tct	att	tta	caa	gca	caa	gag	aga	gca	aaa	336
Gln	Arg	Ile	Arg	Glu	Lys	Ser	Ile	Leu	Gln	Ala	Gln	Glu	Arg	Ala	Lys	
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gaa	gct	aca	gaa	gca	aaa	gct	gca	gca	aag	cgg	gaa	gat	caa	aaa	tat	384
Glu	Ala	Thr	Glu	Ala	Lys	Ala	Ala	Ala	Lys	Arg	Glu	Asp	Gln	Lys	Tyr	
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gca	cta	agt	gtc	atg	atg	aag	att	gaa	gaa	gaa	gag	agg	aaa	aaa	ata	432
Ala	Leu	Ser	Val	Met	Met	Lys	Ile	Glu	Glu	Glu	Glu	Arg	Lys	Lys	Ile	
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gaa	gat	atg	aaa	gaa	aat	gaa	cgg	ata	aaa	gcc	act	aaa	gaa	ttg	gaa	480
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Ala Trp Lys Glu Tyr Gln Arg Lys Ala Glu Glu Gln Lys Lys Ile Gln	
165 170 175	
aga gaa gag aaa tta tgt caa aaa gaa aag caa att aaa gaa gaa aga	576
Arg Glu Glu Lys Leu Cys Gln Lys Glu Lys Gln Ile Lys Glu Glu Arg	
180 185 190	
aaa aaa ata aaa tat aag agt ctt act aga aat ttg gca tct aga aat	624
Lys Lys Ile Lys Tyr Lys Ser Leu Thr Arg Asn Leu Ala Ser Arg Asn	
195 200 205	
ctt gct cca aaa ggg aga aat tca gaa aat ata ttt act gag aag tta	672
Leu Ala Pro Lys Gly Arg Asn Ser Glu Asn Ile Phe Thr Glu Lys Leu	
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aag gaa gac agt att cct gct cct cgc tct gtt ggc agt att aaa atc	720
Lys Glu Asp Ser Ile Pro Ala Pro Arg Ser Val Gly Ser Ile Lys Ile	
225 230 235 240	
aac ttt acc cct cga gta ttc cca aca gct ctt cgt gaa tca caa gta	768
Asn Phe Thr Pro Arg Val Phe Pro Thr Ala Leu Arg Glu Ser Gln Val	
245 250 255	
gca gaa gag gag gag tgg cta cac aaa caa gct gag gca cga aga gca	816
Ala Glu Glu Glu Glu Trp Leu His Lys Gln Ala Glu Ala Arg Arg Ala	
260 265 270	
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Met Asn Thr Asp Ile Ala Glu Leu Cys Asp Leu Lys Glu Glu Glu Lys	
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aac cca gaa tgg ttg aag gat aaa gga aac aaa ttg ttt gca aca gaa	912
Asn Pro Glu Trp Leu Lys Asp Lys Gly Asn Lys Leu Phe Ala Thr Glu	
290 295 300	
aac tat ttg gca gct atc aat gca tat aat tta gcc ata aga cta aat	960
Asn Tyr Leu Ala Ala Ile Asn Ala Tyr Asn Leu Ala Ile Arg Leu Asn	
305 310 315 320	
aat aag atg cca cta ttg tat ttg aac cgg gct gct tgc cac cta aaa	1008
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325 330 335	
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Leu Lys Asn Leu His Lys Ala Ile Glu Asp Ser Ser Lys Ala Leu Glu	
340 345 350	
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Leu Leu Met Pro Pro Val Thr Asp Asn Ala Asn Ala Arg Met Lys Ala	
355 360 365	
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His Val Arg Arg Gly Thr Ala Phe Cys Gln Leu Glu Leu Tyr Val Glu	
370 375 380	

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 385 390 395 400

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gaa cta aaa tct taa 1263
 Glu Leu Lys Ser
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 <212> PRT
 <213> Pan troglodytes

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 35 40 45
 Phe Glu Ala Phe Leu Tyr Ala Pro Ile Asp Asp Glu Ser Ser Lys Ala
 50 55 60
 Lys Ile Gly Asn Asp Thr Ile Val Phe Thr Leu Tyr Lys Lys Glu Ala
 65 70 75 80
 Ala Met Trp Glu Thr Leu Ser Val Thr Gly Val Asp Lys Glu Met Met
 85 90 95
 Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Arg Ala Lys
 100 105 110
 Glu Ala Thr Glu Ala Lys Ala Ala Lys Arg Glu Asp Gln Lys Tyr
 115 120 125
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 Glu Asp Met Lys Glu Asn Glu Arg Ile Lys Ala Thr Lys Glu Leu Glu
 145 150 155 160
 Ala Trp Lys Glu Tyr Gln Arg Lys Ala Glu Glu Gln Lys Lys Ile Gln
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 Arg Glu Glu Lys Leu Cys Gln Lys Glu Lys Gln Ile Lys Glu Glu Arg
 180 185 190
 Lys Lys Ile Lys Tyr Lys Ser Leu Thr Arg Asn Leu Ala Ser Arg Asn
 195 200 205

Leu Ala Pro Lys Gly Arg Asn Ser Glu Asn Ile Phe Thr Glu Lys Leu
 210 215 220
 Lys Glu Asp Ser Ile Pro Ala Pro Arg Ser Val Gly Ser Ile Lys Ile
 225 230 235 240
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 245 250 255
 Ala Glu Glu Glu Glu Trp Leu His Lys Gln Ala Glu Ala Arg Arg Ala
 260 265 270
 Met Asn Thr Asp Ile Ala Glu Leu Cys Asp Leu Lys Glu Glu Glu Lys
 275 280 285
 Asn Pro Glu Trp Leu Lys Asp Lys Gly Asn Lys Leu Phe Ala Thr Glu
 290 295 300
 Asn Tyr Leu Ala Ala Ile Asn Ala Tyr Asn Leu Ala Ile Arg Leu Asn
 305 310 315 320
 Asn Lys Met Pro Leu Leu Tyr Leu Asn Arg Ala Ala Cys His Leu Lys
 325 330 335
 Leu Lys Asn Leu His Lys Ala Ile Glu Asp Ser Ser Lys Ala Leu Glu
 340 345 350
 Leu Leu Met Pro Pro Val Thr Asp Asn Ala Asn Ala Arg Met Lys Ala
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 His Val Arg Arg Gly Thr Ala Phe Cys Gln Leu Glu Leu Tyr Val Glu
 370 375 380
 Gly Leu Gln Asp Tyr Glu Ala Ala Leu Lys Ile Asp Pro Ser Asn Lys
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 Glu Leu Lys Ser
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 <212> DNA
 <213> Gorilla gorilla

<220>
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 <222> (1)..(1260)

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Val Phe Cys Thr Glu Asn Tyr Leu Lys Val Asn Phe Pro Pro Phe Leu				
35 40 45				
ttt gag gca ttt ctt tat gct ccc ata gac gat gag agc agc aaa gca	192			
Phe Glu Ala Phe Leu Tyr Ala Pro Ile Asp Asp Glu Ser Ser Lys Ala				
50 55 60				
aag att ggg aat gac acc att gtc ttc acc ttg tat aaa aaa gaa gcg	240			
Lys Ile Gly Asn Asp Thr Ile Val Phe Thr Leu Tyr Lys Lys Glu Ala				
65 70 75 80				
gcc atg tgg gag acc ctt tct gtg acg ggt gtt gac aaa gag atg atg	288			
Ala Met Trp Glu Thr Leu Ser Val Thr Gly Val Asp Lys Glu Met Met				
85 90 95				
caa aga att aga gaa aaa tct att tta caa gca caa gag aga gca aaa	336			
Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Arg Ala Lys				
100 105 110				
gaa gct aca gaa gca aaa gct gca gca aag cgg gaa gat caa aaa tat	384			
Glu Ala Thr Glu Ala Lys Ala Ala Lys Arg Glu Asp Gln Lys Tyr				
115 120 125				
gca cta agt gtc atg atg aag att gaa gaa gaa gag agg aaa aaa ata	432			
Ala Leu Ser Val Met Met Lys Ile Glu Glu Glu Glu Arg Lys Lys Ile				
130 135 140				
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Glu Asp Met Lys Glu Asn Glu Arg Ile Lys Ala Thr Lys Glu Leu Glu				
145 150 155 160				
gcc tgg aaa gaa tat caa aga aaa gct gag gag caa aaa gaa att cag	528			
Ala Trp Lys Glu Tyr Gln Arg Lys Ala Glu Glu Gln Lys Glu Ile Gln				
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aga gaa gag aag tta tgt caa aaa gaa aag caa att aaa gaa gaa aga	576			
Arg Glu Glu Lys Leu Cys Gln Lys Glu Lys Gln Ile Lys Glu Glu Arg				
180 185 190				
aaa aaa tta aaa tat aag agt ctt act aga aat ttg gca tct aga aat	624			
Lys Lys Leu Lys Tyr Lys Ser Leu Thr Arg Asn Leu Ala Ser Arg Asn				
195 200 205				
ctt gct cca aaa ggg aga aat tca gaa aat ata ttt act gag aag tta	672			
Leu Ala Pro Lys Gly Arg Asn Ser Glu Asn Ile Phe Thr Glu Lys Leu				
210 215 220				
aag gaa gac agt att cct gct cct cgc tct gtt ggc agt att aaa atc	720			
Lys Glu Asp Ser Ile Pro Ala Pro Arg Ser Val Gly Ser Ile Lys Ile				
225 230 235 240				

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Asn Phe Thr Pro Arg Val Phe Pro Thr Ala Leu Arg Glu Ser Gln Val	
245 250 255	
gca gaa gag gag gag tgg cta cac aaa caa gct gag gca cga aga gca	816
Ala Glu Glu Glu Glu Trp Leu His Lys Gln Ala Glu Ala Arg Arg Ala	
260 265 270	
atg aat act gac ata gct gaa ctt tgc gat tta aaa gaa gaa gaa aag	864
Met Asn Thr Asp Ile Ala Glu Leu Cys Asp Leu Lys Glu Glu Glu Lys	
275 280 285	
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Asn Pro Glu Trp Leu Lys Asp Lys Gly Asn Lys Leu Phe Ala Thr Glu	
290 295 300	
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305 310 315 320	
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Asn Lys Met Pro Leu Leu Tyr Leu Asn Arg Ala Ala Cys His Leu Lys	
325 330 335	
cta aaa aac tta cac aag gct att gaa gat tct tct aag gca ctg gaa	1056
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340 345 350	
tta ttg atg cca cct gtt aca gac aat gct aat gca aga atg aag gca	1104
Leu Leu Met Pro Pro Val Thr Asp Asn Ala Asn Ala Arg Met Lys Ala	
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cat gta cga cgt gga aca gca ttc tgt caa cta gaa ttg tat gta gaa	1152
His Val Arg Arg Gly Thr Ala Phe Cys Gln Leu Glu Leu Tyr Val Glu	
370 375 380	
ggc cta cag gat tat gaa gcg gca ctt aag att gat cca tcc aac aaa	1200
Gly Leu Gln Asp Tyr Glu Ala Ala Leu Lys Ile Asp Pro Ser Asn Lys	
385 390 395 400	
att gta caa att gat gct gag aag att cgg aat gta att caa gga aca	1248
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Glu Leu Lys Ser	
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<211> 420

<212> PRT

<213> Gorilla gorilla

<400> 16

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Phe Glu Ala Phe Leu Tyr Ala Pro Ile Asp Asp Glu Ser Ser Lys Ala	50	55	60
Lys Ile Gly Asn Asp Thr Ile Val Phe Thr Leu Tyr Lys Lys Glu Ala	65	70	75
Ala Met Trp Glu Thr Leu Ser Val Thr Gly Val Asp Lys Glu Met Met	85	90	95
Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Arg Ala Lys	100	105	110
Glu Ala Thr Glu Ala Lys Ala Ala Ala Lys Arg Glu Asp Gln Lys Tyr	115	120	125
Ala Leu Ser Val Met Met Lys Ile Glu Glu Glu Glu Arg Lys Lys Ile	130	135	140
Glu Asp Met Lys Glu Asn Glu Arg Ile Lys Ala Thr Lys Glu Leu Glu	145	150	155
Ala Trp Lys Glu Tyr Gln Arg Lys Ala Glu Glu Gln Lys Glu Ile Gln	165	170	175
Arg Glu Glu Lys Leu Cys Gln Lys Glu Lys Gln Ile Lys Glu Glu Arg	180	185	190
Lys Lys Leu Lys Tyr Lys Ser Leu Thr Arg Asn Leu Ala Ser Arg Asn	195	200	205
Leu Ala Pro Lys Gly Arg Asn Ser Glu Asn Ile Phe Thr Glu Lys Leu	210	215	220
Lys Glu Asp Ser Ile Pro Ala Pro Arg Ser Val Gly Ser Ile Lys Ile	225	230	235
Asn Phe Thr Pro Arg Val Phe Pro Thr Ala Leu Arg Glu Ser Gln Val	245	250	255
Ala Glu Glu Glu Glu Trp Leu His Lys Gln Ala Glu Ala Arg Arg Ala	260	265	270
Met Asn Thr Asp Ile Ala Glu Leu Cys Asp Leu Lys Glu Glu Glu Lys	275	280	285
Asn Pro Glu Trp Leu Lys Asp Lys Gly Asn Lys Leu Phe Ala Thr Glu	290	295	300
Asn Tyr Leu Ala Ala Ile Asn Ala Tyr Asn Leu Ala Ile Arg Leu Asn			

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Asn Lys Met Pro	Leu Leu Tyr Leu	Asn Arg Ala Ala Cys His	Leu Lys			
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Leu Lys Asn Leu	His Lys Ala Ile	Glu Asp Ser Ser	Lys Ala Leu Glu			
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Leu Leu Met Pro	Pro Val Thr Asp	Asn Ala Asn Ala	Arg Met Lys Ala			
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His Val Arg Arg	Gly Thr Ala Phe	Cys Gln Leu Glu	Leu Tyr Val Glu			
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Gly Leu Gln Asp	Tyr Glu Ala Ala	Leu Lys Ile Asp	Pro Ser Asn Lys			
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Val Phe Leu Ser Leu Pro Leu Lys Gly Val Cys Val Arg Asp Thr Asp	
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gtg ttc tgc acg gaa aac tat ctg aag gtc aac ttt cct cca ttt tta	144
Val Phe Cys Thr Glu Asn Tyr Leu Lys Val Asn Phe Pro Pro Phe Leu	
35 40 45	
ttt gag gca ttt ctt tat gct ccc ata gac gat gag agc agc aaa gca	192
Phe Glu Ala Phe Leu Tyr Ala Pro Ile Asp Asp Glu Ser Ser Lys Ala	
50 55 60	
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Lys Ile Gly Asn Asp Thr Ile Val Phe Thr Leu Tyr Lys Lys Glu Ala	
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gcc atg tgg gag acc ctt tct gtg acg ggt gtt gac aaa gag acg atg	288
Ala Met Trp Glu Thr Leu Ser Val Thr Gly Val Asp Lys Glu Thr Met	

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caa	aga	att	aga	gaa	aaa	tct	att	tta	caa	gca	caa	gag	aga	gca	aaa	336				
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			100				105						110							
gaa	gct	aca	gaa	gca	aaa	gct	gca	gca	aag	cgg	gaa	gat	caa	aaa	tat	384				
Glu	Ala	Thr	Glu	Ala	Lys	Ala	Ala	Ala	Lys	Arg	Glu	Asp	Gln	Lys	Tyr					
			115				120						125							
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Ala	Leu	Ser	Val	Met	Met	Lys	Ile	Glu	Glu	Glu	Glu	Arg	Lys	Lys	Ile					
			130				135						140							
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Glu	Asp	Met	Lys	Glu	Asn	Glu	Arg	Ile	Lys	Ala	Thr	Lys	Glu	Leu	Glu					
145			150						155			160								
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Ala	Trp	Lys	Glu	Tyr	Gln	Arg	Lys	Ala	Glu	Glu	His	Lys	Lys	Ile	Gln					
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Arg	Glu	Glu	Lys	Leu	Cys	Gln	Lys	Glu	Lys	Gln	Ile	Lys	Glu	Glu	Arg					
			180						185			190								
aaa	aaa	tta	aaa	tac	aag	agt	ctt	act	aga	aat	tcg	gca	tct	aga	aac	624				
Lys	Lys	Leu	Lys	Tyr	Lys	Ser	Leu	Thr	Arg	Asn	Ser	Ala	Ser	Arg	Asn					
195						200						205								
ctt	gct	cca	aaa	gga	aga	aat	tca	gaa	aat	ata	ttt	act	gag	aag	tta	672				
Leu	Ala	Pro	Lys	Gly	Arg	Asn	Ser	Glu	Asn	Ile	Phe	Thr	Glu	Lys	Leu					
210						215						220								
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Lys	Glu	Asp	Ser	Ile	Pro	Ala	Pro	Arg	Ser	Val	Gly	Ser	Ile	Lys	Ile					
225			230						235			240								
aac	ttt	acc	cct	cga	gta	ttc	cca	aca	gct	ctt	cgt	gaa	tca	caa	gta	768				
Asn	Phe	Thr	Pro	Arg	Val	Phe	Pro	Thr	Ala	Leu	Arg	Glu	Ser	Gln	Val					
			245						250			255								
gca	gaa	gag	gag	gag	tg	cta	cac	aaa	caa	gct	gag	gca	cga	aga	gca	816				
Ala	Glu	Glu	Glu	Glu	Trp	Leu	His	Lys	Gln	Ala	Glu	Ala	Arg	Arg	Ala					
			260						265			270								
atg	aat	act	gac	ata	gct	gaa	ctt	tgc	gat	tta	aaa	gaa	gaa	gaa	aag	864				
Met	Asn	Thr	Asp	Ile	Ala	Glu	Leu	Cys	Asp	Leu	Lys	Glu	Glu	Glu	Lys					
275						280						285								
aac	cca	gaa	tg	ttg	aag	gat	aaa	gga	aac	aaa	ttg	ttt	gca	aca	gaa	912				
Asn	Pro	Glu	Trp	Leu	Lys	Asp	Lys	Gly	Asn	Lys	Leu	Phe	Ala	Thr	Glu					
290						295						300								
aac	tat	ttg	gca	gct	atc	aat	gca	tat	aat	tta	gcc	ata	aga	cta	aat	960				
Asn	Tyr	Leu	Ala	Ala	Ile	Asn	Ala	Tyr	Asn	Leu	Ala	Ile	Arg	Leu	Asn					
305			310						315			320								

aat aag atg cca cta ttg tat ttg aac cgg gct gct tgc cac cta aaa	1008
Asn Lys Met Pro Leu Leu Tyr Leu Asn Arg Ala Ala Cys His Leu Lys	
325 330 335	

cta aaa aac tta cac aag gct att gaa gat tct tct aag gca ctg gaa	1056
Leu Lys Asn Leu His Lys Ala Ile Glu Asp Ser Ser Lys Ala Leu Glu	
340 345 350	

tta ttg atg cca cct gtt aca gac aat gct aat gca aga atg aag gca	1104
Leu Leu Met Pro Pro Val Thr Asp Asn Ala Asn Ala Arg Met Lys Ala	
355 360 365	

cat gta cga cgt gga aca gca ttc tgt caa cta gaa ttg tat gta gaa	1152
His Val Arg Arg Gly Thr Ala Phe Cys Gln Leu Glu Leu Tyr Val Glu	
370 375 380	

ggc cta cag gat tat gaa gcg gca ctt aag att gat cca tcc aac aaa	1200
Gly Leu Gln Asp Tyr Glu Ala Ala Leu Lys Ile Asp Pro Ser Asn Lys	
385 390 395 400	

att gta caa att gat gct gag aag att cgg aat gta att caa gga aca	1248
Ile Val Gln Ile Asp Ala Glu Lys Ile Arg Asn Val Ile Gln Gly Thr	
405 410 415	

gaa cta aaa tct taa	1263
Glu Leu Lys Ser	
420	

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 <213> Pongo pygmaeus

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Val Phe Cys Thr Glu Asn Tyr Leu Lys Val Asn Phe Pro Pro Phe Leu	
35 40 45	
Phe Glu Ala Phe Leu Tyr Ala Pro Ile Asp Asp Glu Ser Ser Lys Ala	
50 55 60	
Lys Ile Gly Asn Asp Thr Ile Val Phe Thr Leu Tyr Lys Lys Glu Ala	
65 70 75 80	
Ala Met Trp Glu Thr Leu Ser Val Thr Gly Val Asp Lys Glu Thr Met	
85 90 95	
Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Arg Ala Lys	
100 105 110	

Glu	Ala	Thr	Glu	Ala	Lys	Ala	Ala	Ala	Lys	Arg	Glu	Asp	Gln	Lys	Tyr	115	120	125	
Ala	Leu	Ser	Val	Met	Met	Lys	Ile	Glu	Glu	Glu	Glu	Arg	Lys	Lys	Ile	130	135	140	
Glu	Asp	Met	Lys	Glu	Asn	Glu	Arg	Ile	Lys	Ala	Thr	Lys	Glu	Leu	Glu	145	150	155	160
Ala	Trp	Lys	Glu	Tyr	Gln	Arg	Lys	Ala	Glu	Glu	His	Lys	Lys	Ile	Gln	165	170	175	
Arg	Glu	Glu	Lys	Leu	Cys	Gln	Lys	Glu	Lys	Gln	Ile	Lys	Glu	Glu	Arg	180	185	190	
Lys	Lys	Leu	Lys	Tyr	Lys	Ser	Leu	Thr	Arg	Asn	Ser	Ala	Ser	Arg	Asn	195	200	205	
Leu	Ala	Pro	Lys	Gly	Arg	Asn	Ser	Glu	Asn	Ile	Phe	Thr	Glu	Lys	Leu	210	215	220	
Lys	Glu	Asp	Ser	Ile	Pro	Ala	Pro	Arg	Ser	Val	Gly	Ser	Ile	Lys	Ile	225	230	235	240
Asn	Phe	Thr	Pro	Arg	Val	Phe	Pro	Thr	Ala	Leu	Arg	Glu	Ser	Gln	Val	245	250	255	
Ala	Glu	Glu	Glu	Glu	Trp	Leu	His	Lys	Gln	Ala	Glu	Ala	Arg	Arg	Ala	260	265	270	
Met	Asn	Thr	Asp	Ile	Ala	Glu	Leu	Cys	Asp	Leu	Lys	Glu	Glu	Glu	Lys	275	280	285	
Asn	Pro	Glu	Trp	Leu	Lys	Asp	Lys	Gly	Asn	Lys	Leu	Phe	Ala	Thr	Glu	290	295	300	
Asn	Tyr	Leu	Ala	Ala	Ile	Asn	Ala	Tyr	Asn	Leu	Ala	Ile	Arg	Leu	Asn	305	310	315	320
Asn	Lys	Met	Pro	Leu	Leu	Tyr	Leu	Asn	Arg	Ala	Ala	Cys	His	Leu	Lys	325	330	335	
Leu	Lys	Asn	Leu	His	Lys	Ala	Ile	Glu	Asp	Ser	Ser	Lys	Ala	Leu	Glu	340	345	350	
Leu	Leu	Met	Pro	Pro	Val	Thr	Asp	Asn	Ala	Asn	Ala	Arg	Met	Lys	Ala	355	360	365	
His	Val	Arg	Arg	Gly	Thr	Ala	Phe	Cys	Gln	Leu	Glu	Leu	Tyr	Val	Glu	370	375	380	
Gly	Leu	Gln	Asp	Tyr	Glu	Ala	Ala	Leu	Lys	Ile	Asp	Pro	Ser	Asn	Lys	385	390	395	400
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Glu Leu Lys Ser
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<213> Pan paniscus

<220>
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1 5 10 15

gtc ttt ctg tct ctg ccc ctc aaa ggc gtg tgc gtc aga gac acg gac 96
Val Phe Leu Ser Leu Pro Leu Lys Gly Val Cys Val Arg Asp Thr Asp
20 25 30

gtg ttc tgc acg gaa aac tat ctg aag gtc aac ttt cct cca ttt tta 144
Val Phe Cys Thr Glu Asn Tyr Leu Lys Val Asn Phe Pro Pro Phe Leu
35 40 45

ttt gag gca ttt ctt tat gct ccc ata gac gat gag agc agc aaa gca 192
Phe Glu Ala Phe Leu Tyr Ala Pro Ile Asp Asp Glu Ser Ser Lys Ala
50 55 60

aag att ggg aat gac acc att gtc ttc acc ttg tat aaa aaa gaa gcg 240
Lys Ile Gly Asn Asp Thr Ile Val Phe Thr Leu Tyr Lys Lys Glu Ala
65 70 75 80

gcc atg tgg gag acc ctt tct gtg acg ggt gtt gac aaa gag atg atg 288
Ala Met Trp Glu Thr Leu Ser Val Thr Gly Val Asp Lys Glu Met Met
85 90 95

caa aga att aga gaa aaa tct att tta caa gca caa gag aga gca aaa 336
Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Arg Ala Lys
100 105 110

gaa gct aca gaa gca aaa gct gca gca aag cgg gaa gat caa aaa tat 384
Glu Ala Thr Glu Ala Lys Ala Ala Ala Lys Arg Glu Asp Gln Lys Tyr
115 120 125

gca cta agt gtc atg atg aag att gaa gaa gaa gag agg aaa aaa ata 432
Ala Leu Ser Val Met Met Lys Ile Glu Glu Glu Glu Arg Lys Lys Ile
130 135 140

gaa gat atg aaa gaa aat gaa cgg ata aaa gcc act aaa gaa ttg gaa 480
Glu Asp Met Lys Glu Asn Glu Arg Ile Lys Ala Thr Lys Glu Leu Glu
145 150 155 160

gcc tgg aaa gaa tat caa aga aaa gct gag gag caa aaa aaa att cag 528
Ala Trp Lys Glu Tyr Gln Arg Lys Ala Glu Glu Gln Lys Lys Ile Gln

165								170					175				
aga	gaa	gag	aaa	tta	tgt	caa	aaa	gaa	aag	caa	att	aaa	gaa	gaa	aga	576	
Arg	Glu	Glu	Lys	Leu	Cys	Gln	Lys	Glu	Lys	Gln	Ile	Lys	Glu	Glu	Arg		
			180				185						190				
aaa	aaa	ata	aaa	tat	aag	agt	ctt	act	aga	aat	ttg	gca	tct	aga	aat	624	
Lys	Lys	Ile	Lys	Tyr	Lys	Ser	Leu	Thr	Arg	Asn	Leu	Ala	Ser	Arg	Asn		
			195				200						205				
ctt	gct	cca	aaa	ggg	aga	aat	tca	gaa	aat	ata	ttt	act	gag	aag	tta	672	
Leu	Ala	Pro	Lys	Gly	Arg	Asn	Ser	Glu	Asn	Ile	Phe	Thr	Glu	Lys	Leu		
		210				215						220					
aag	gaa	gac	agt	att	cct	gct	cct	cgc	tct	gtt	ggc	agt	att	aaa	atc	720	
Lys	Glu	Asp	Ser	Ile	Pro	Ala	Pro	Arg	Ser	Val	Gly	Ser	Ile	Lys	Ile		
225					230						235				240		
aac	ttt	acc	cct	cga	gta	ttc	cca	aca	gct	ctt	cgt	gaa	tca	caa	gta	768	
Asn	Phe	Thr	Pro	Arg	Val	Phe	Pro	Thr	Ala	Leu	Arg	Glu	Ser	Gln	Val		
			245						250						255		
gca	gaa	gag	gag	gag	tgg	ctg	cac	aaa	caa	gct	gag	gca	cga	aga	gca	816	
Ala	Glu	Glu	Glu	Glu	Trp	Leu	His	Lys	Gln	Ala	Glu	Ala	Arg	Arg	Ala		
			260						265						270		
atg	aat	act	gac	ata	gct	gaa	ctt	tgc	gat	tta	aaa	gaa	gaa	gaa	aag	864	
Met	Asn	Thr	Asp	Ile	Ala	Glu	Leu	Cys	Asp	Leu	Lys	Glu	Glu	Glu	Lys		
			275						280						285		
aac	cca	gaa	tgg	ttg	aag	gat	aaa	gga	aac	aaa	ttg	ttt	gca	aca	gaa	912	
Asn	Pro	Glu	Trp	Leu	Lys	Asp	Lys	Gly	Asn	Lys	Leu	Phe	Ala	Thr	Glu		
290					295						300						
aac	tat	ttg	gca	gct	atc	aat	gca	tat	aat	tta	gcc	ata	aga	cta	aat	960	
Asn	Tyr	Leu	Ala	Ala	Ile	Asn	Ala	Tyr	Asn	Leu	Ala	Ile	Arg	Leu	Asn		
305					310						315					320	
aat	aag	atg	cca	cta	ttg	tat	ttg	aac	cgg	gct	gct	tgc	cac	cta	aaa	1008	
Asn	Lys	Met	Pro	Leu	Leu	Tyr	Leu	Asn	Arg	Ala	Ala	Cys	His	Leu	Lys		
			325						330						335		
cta	aaa	aac	tta	cac	aag	gct	att	gaa	gat	tct	tct	aag	gca	ctg	gaa	1056	
Leu	Lys	Asn	Leu	His	Lys	Ala	Ile	Glu	Asp	Ser	Ser	Lys	Ala	Leu	Glu		
			340						345						350		
tta	ttg	atg	cca	cct	gtt	aca	gac	aat	gct	aat	gca	aga	atg	aag	gca	1104	
Leu	Leu	Met	Pro	Pro	Val	Thr	Asp	Asn	Ala	Asn	Ala	Arg	Met	Lys	Ala		
			355						360						365		
cat	gta	cga	cgt	gga	aca	gca	ttc	tgt	caa	cta	gaa	ttg	tat	gta	gaa	1152	
His	Val	Arg	Arg	Gly	Thr	Ala	Phe	Cys	Gln	Leu	Glu	Leu	Tyr	Val	Glu		
370					375						380						
ggc	cta	cag	gat	tat	gaa	gcg	gca	ctt	aag	att	gat	cca	tcc	aac	aaa	1200	
Gly	Leu	Gln	Asp	Tyr	Glu	Ala	Ala	Leu	Lys	Ile	Asp	Pro	Ser	Asn	Lys		
385					390						395					400	

att gta caa att gat gct gag aag att cgg aat gta att caa gga aca	1248
Ile Val Gln Ile Asp Ala Glu Lys Ile Arg Asn Val Ile Gln Gly Thr	
405 410 415	

gaa cta aaa tct taa	1263
Glu Leu Lys Ser	
420	

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 <213> Pan paniscus

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Val Phe Cys Thr Glu Asn Tyr Leu Lys Val Asn Phe Pro Pro Phe Leu	
35 40 45	
Phe Glu Ala Phe Leu Tyr Ala Pro Ile Asp Asp Glu Ser Ser Lys Ala	
50 55 60	
Lys Ile Gly Asn Asp Thr Ile Val Phe Thr Leu Tyr Lys Lys Glu Ala	
65 70 75 80	
Ala Met Trp Glu Thr Leu Ser Val Thr Gly Val Asp Lys Glu Met Met	
85 90 95	
Gln Arg Ile Arg Glu Lys Ser Ile Leu Gln Ala Gln Glu Arg Ala Lys	
100 105 110	
Glu Ala Thr Glu Ala Lys Ala Ala Ala Lys Arg Glu Asp Gln Lys Tyr	
115 120 125	
Ala Leu Ser Val Met Met Lys Ile Glu Glu Glu Glu Arg Lys Lys Ile	
130 135 140	
Glu Asp Met Lys Glu Asn Glu Arg Ile Lys Ala Thr Lys Glu Leu Glu	
145 150 155 160	
Ala Trp Lys Glu Tyr Gln Arg Lys Ala Glu Glu Gln Lys Lys Ile Gln	
165 170 175	
Arg Glu Glu Lys Leu Cys Gln Lys Glu Lys Gln Ile Lys Glu Glu Arg	
180 185 190	
Lys Lys Ile Lys Tyr Lys Ser Leu Thr Arg Asn Leu Ala Ser Arg Asn	
195 200 205	
Leu Ala Pro Lys Gly Arg Asn Ser Glu Asn Ile Phe Thr Glu Lys Leu	
210 215 220	

Lys Glu Asp Ser Ile Pro Ala Pro Arg Ser Val Gly Ser Ile Lys Ile
 225 230 235 240
 Asn Phe Thr Pro Arg Val Phe Pro Thr Ala Leu Arg Glu Ser Gln Val
 245 250 255
 Ala Glu Glu Glu Glu Trp Leu His Lys Gln Ala Glu Ala Arg Arg Ala
 260 265 270
 Met Asn Thr Asp Ile Ala Glu Leu Cys Asp Leu Lys Glu Glu Glu Lys
 275 280 285
 Asn Pro Glu Trp Leu Lys Asp Lys Gly Asn Lys Leu Phe Ala Thr Glu
 290 295 300
 Asn Tyr Leu Ala Ala Ile Asn Ala Tyr Asn Leu Ala Ile Arg Leu Asn
 305 310 315 320
 Asn Lys Met Pro Leu Leu Tyr Leu Asn Arg Ala Ala Cys His Leu Lys
 325 330 335
 Leu Lys Asn Leu His Lys Ala Ile Glu Asp Ser Ser Lys Ala Leu Glu
 340 345 350
 Leu Leu Met Pro Pro Val Thr Asp Asn Ala Asn Ala Arg Met Lys Ala
 355 360 365
 His Val Arg Arg Gly Thr Ala Phe Cys Gln Leu Glu Leu Tyr Val Glu
 370 375 380
 Gly Leu Gln Asp Tyr Glu Ala Ala Leu Lys Ile Asp Pro Ser Asn Lys
 385 390 395 400
 Ile Val Gln Ile Asp Ala Glu Lys Ile Arg Asn Val Ile Gln Gly Thr
 405 410 415
 Glu Leu Lys Ser
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 <220>
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 <210> 24
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 <400> 24
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 <210> 25
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<210> 35
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<210> 42

<211> 27

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<223> PCR Primer 126403-F

<400> 42

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27